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1	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Asp	Ser	Pro	Leu	Gly	Gly	Gly
1	CAG	AGG	TTG	CCC	CGG	ATG	CAG	GAG	GAT	TCC	CCC	TTG	GGA	GGA	GGC
16	Ser	Ser	Gly	Glu	Asp	Asp	Pro	Leu	Gly	Glu	Glu	Asp	Leu	Pro	Ser
46	TCT	TCT	GGG	GAA	GAT	GAC	CCA	CTG	GGC	GAG	GAG	GAT	CTG	CCC	AGT
31	Glu	Glu	Asp	Ser	Pro	Arg	Glu	Glu	Asp	Pro	Pro	Gly	Glu	Glu	Asp
91	GAA	GAG	GAT	TCA	CCC	AGA	GAG	GAG	GAT	CCA	CCC	GGA	GAG	GAG	GAT
46	Leu	Pro	Gly	Glu	Glu	Asp	Leu	Pro	Gly	Glu	Glu	Asp	Leu	Pro	Glu
136	CTA	CCT	GGA	GAG	GAG	GAT	CTA	CCT	GGA	GAG	GAG	GAT	CTA	CCT	GAA
61	Val	Lys	Pro	Lys	Ser	Glu	Glu	Glu	Gly	Ser	Leu	Lys	Leu	Glu	Asp
181	GTT	AAG	CCT	AAA	TCA	GAA	GAA	GAG	GGC	TCC	CTG	AAG	TTA	GAG	GAT
76	Leu	Pro	Thr	Val	Glu	Ala	Pro	Gly	Asp	Pro	Gln	Glu	Pro	Gln	Asn
226	CTA	CCT	ACT	GTT	GAG	GCT	CCT	GGA	GAT	CCT	CAA	GAA	CCC	CAG	AAT
91	Asn	Ala	His	Arg	Asp	Lys	Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg
271	AAT	GCC	CAC	AGG	GAC	AAA	GAA	GGG	GAT	GAC	CAG	AGT	CAT	TGG	CGC
106	Tyr	Gly	Gly	Asp	Pro	Pro	Trp	Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala
316	TAT	GGA	GGC	GAC	CCG	CCC	TGG	CCC	CGG	GTG	TCC	CCA	GCC	TGC	GCG
121	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp	Ile	Arg	Pro	Gln	Leu	Ala	Ala
361	GGC	CGC	TTC	CAG	TCC	CCG	GTG	GAT	ATC	CGC	CCC	CAG	CTC	GCC	GCC
136	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu	Leu	Leu	Gly	Phe	Gln	Leu
406	TTC	TGC	CCG	GCC	CTG	CGC	CCC	CTG	GAA	CTC	CTG	GGC	TTC	CAG	CTC
151	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn	Asn	Gly	His	Ser	Val
451	CCG	CCG	CTC	CCA	GAA	CTG	CGC	CTG	CGC	AAC	AAT	GGC	CAC	AGT	GTG
166	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala	Leu	Gly	Pro	Gly
496	CAA	CTG	ACC	CTG	CCT	CCT	GGG	CTA	GAG	ATG	GCT	CTG	GGT	CCC	GGG
191	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp	Gly	Ala	Ala
541	CGG	GAG	TAC	CGG	GCT	CTG	CAG	CTG	CAT	CTG	CAC	TGG	GGG	GCT	GCA
196	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	Phe	Pro
586	GGT	CGT	CCG	GGC	TCG	GAG	CAC	ACT	GTG	GAA	GGC	CAC	CGT	TTC	CCT
211	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	Val
631	GCC	GAG	ATC	CAC	GTG	GTT	CAC	CTC	AGC	ACC	GCC	TTT	GCC	AGA	GTT

**FIG.\_1A**

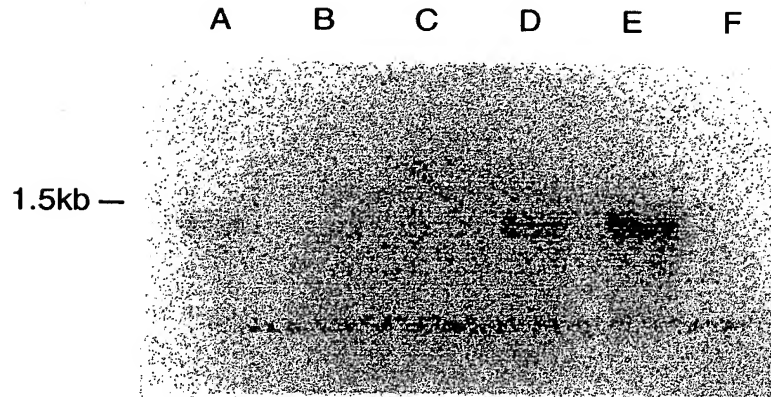
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226 Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala  
 676 GAC GAG GCC TTG GGG CGC CCG GGA GGC CTG GCC GTG TTG GCC GCC  
  
 241 Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu  
 721 TTT CTG GAG GAG GGC CCG GAA GAA AAC AGT GCC TAT GAG CAG TTG  
  
 256 Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln  
 766 CTG TCT CGC TTG GAA GAA ATC GCT GAG GAA GGC TCA GAG ACT CAG  
  
 271 Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser  
 811 GTC CCA GGA CTG GAC ATA TCT GCA CTC CTG CCC TCT GAC TTC AGC  
  
 286 Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala  
 856 CGC TAC TTC CAA TAT GAG GGG TCT CTG ACT ACA CCG CCC TGT GCC  
  
 301 Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser  
 901 CAG GGT GTC ATC TGG ACT GTG TTT AAC CAG ACA GTG ATG CTG AGT  
  
 316 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly  
 946 GCT AAG CAG CTC CAC ACC CTC TCT GAC ACC CTG TGG GGA CCT GGT  
  
 331 Asp Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn  
 991 GAC TCT CGG CTA CAG CTG AAC TTC CGA GCG ACG CAG CCT TTG AAT  
  
 346 Gly Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser  
 1046 GGG CGA GTG ATT GAG GCC TCC TTC CCT GCT GGA GTG GAC AGC AGT  
  
 361 Pro Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala  
 1081 CCT CGG GCT GCT GAG CCA GTC CAG CTG AAT TCC TGC CTG GCT GCT  
  
 376 Gly Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr  
 1126 GGT GAC ATC CTA GCC CTG GTT TTT GGC CTC CTT TTT GCT GTC ACC  
  
 391 Ser Val Ala Phe Leu Val Gln Met Arg Arg Gln His Arg Arg Gly  
 1171 AGC GTC GCG TTC CTT GTG CAG ATG AGA AGG CAG CAC AGA AGG GGA  
  
 406 Thr Lys Gly Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu Thr  
 1216 ACC AAA GGG GGT GTG AGC TAC CGC CCA GCA GAG GTA GCC GAG ACT  
  
 421 Gly Ala  
 1261 GGA GCC TAG AGG CTG GAT CTT GGA GAA TGT GAG AAG CCA GCC AGA  
  
 1306 GGC ATC TGA GGG GGA GCC GGT AAC TGT CCT GTC CTG CTC ATT ATG  
  
 1351 CCA CTT CCT TTT AAC TGC CAA GAA ATT TTT TAA AAT AAA TAT TTA  
  
 1396 TAA T

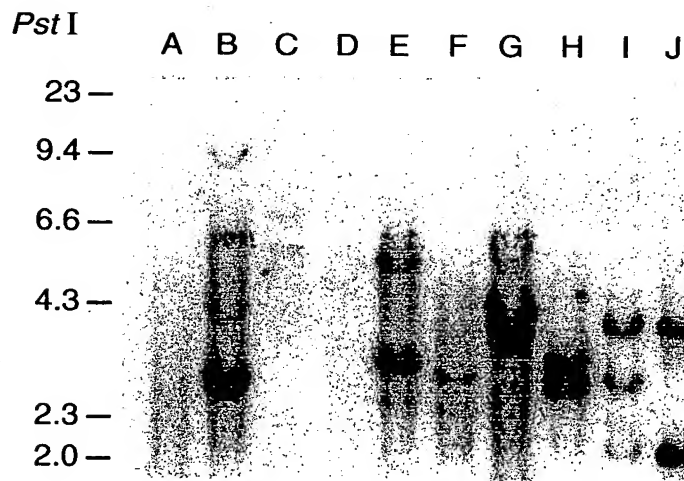
**FIG. 1B**



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**FIG.\_4**

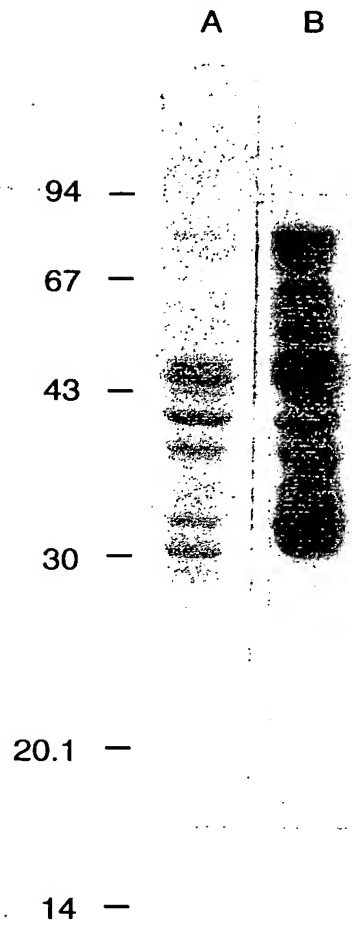


**FIG.\_5**

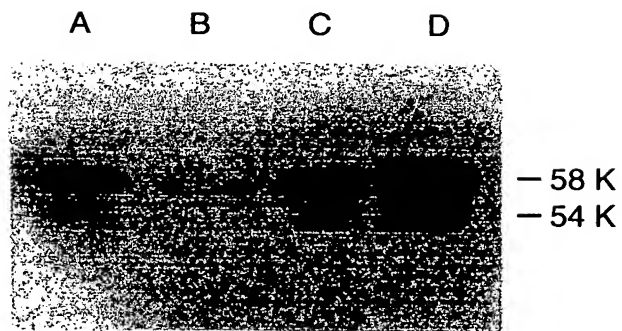


+

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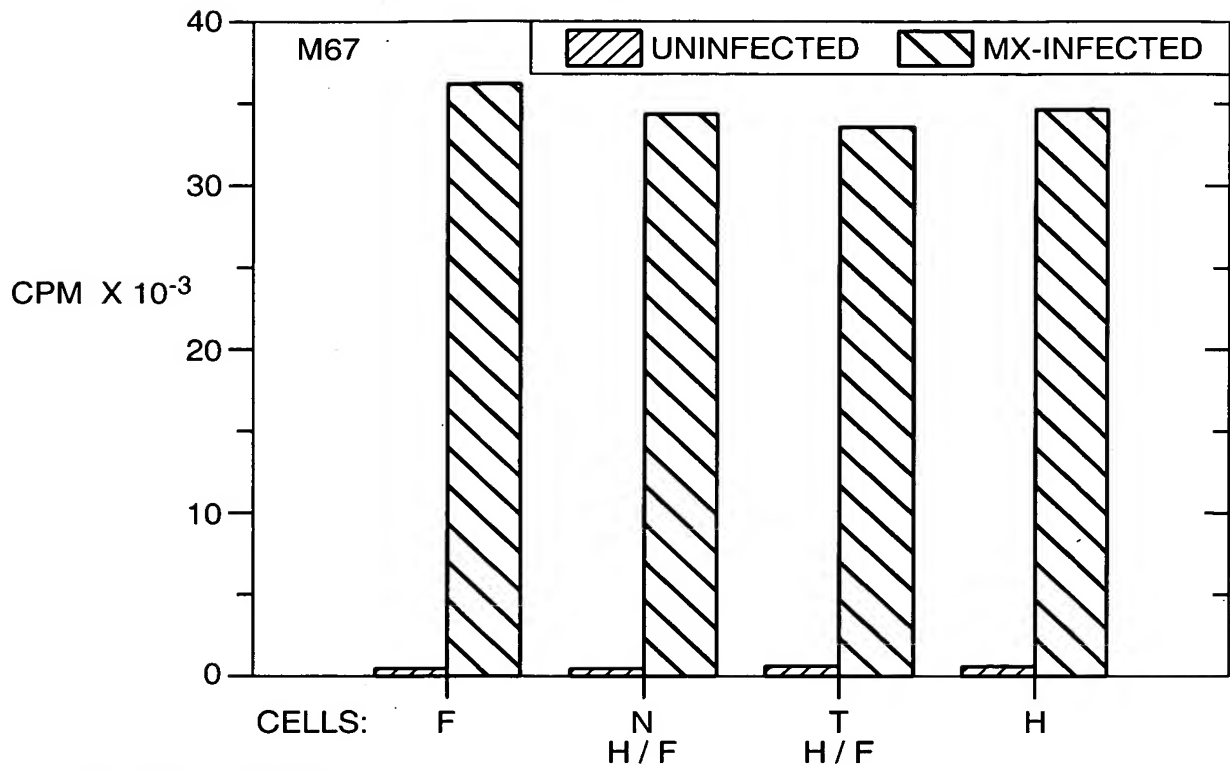
**FIG.\_2**



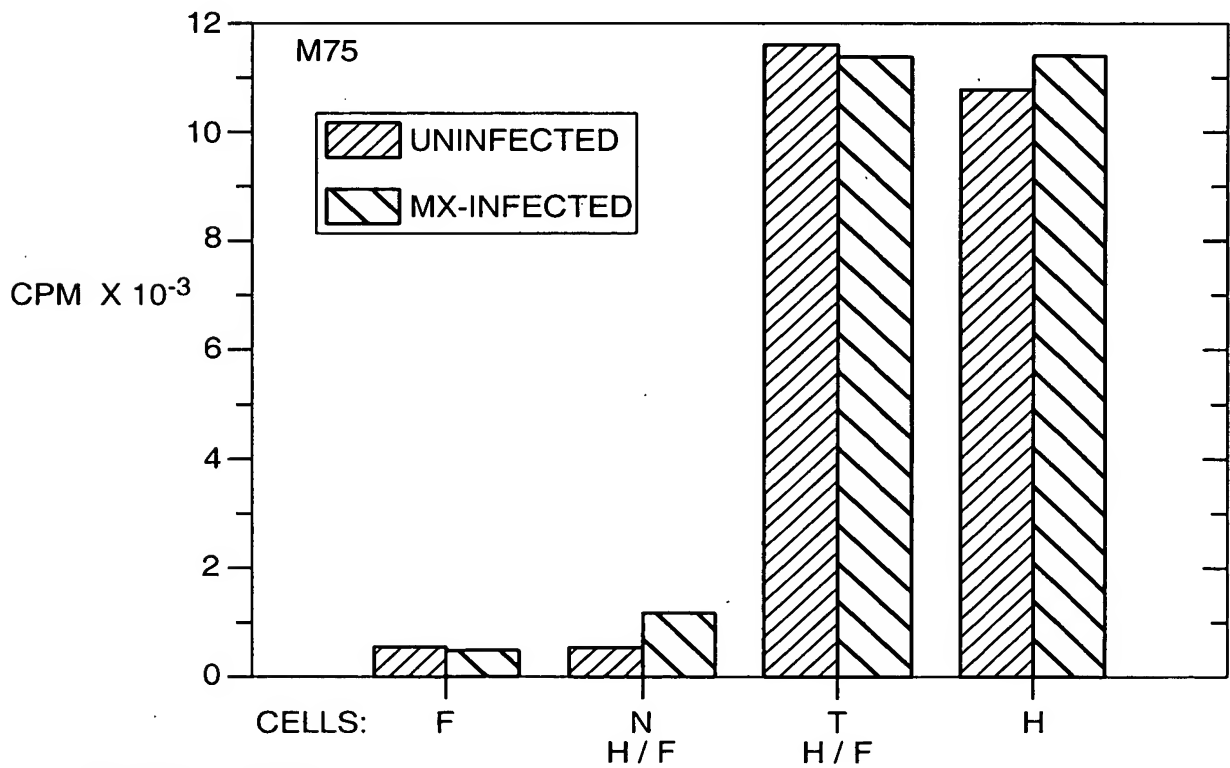
**FIG.\_3**

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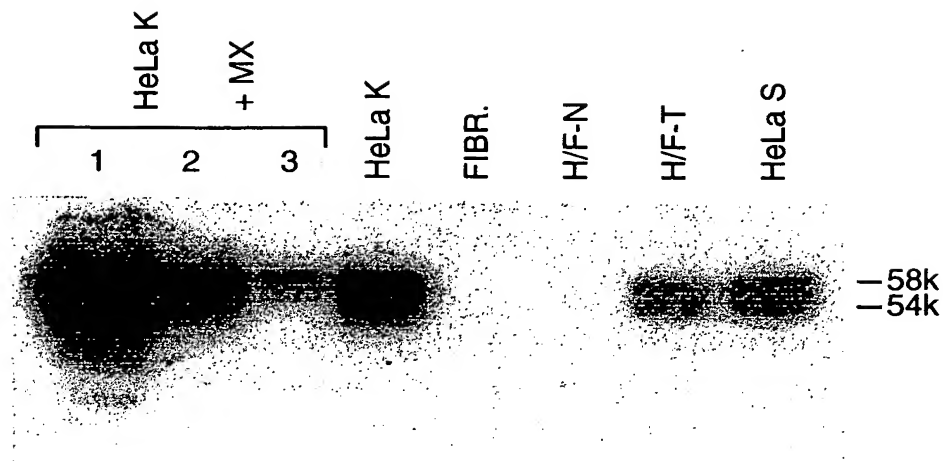


**FIG.\_6A**

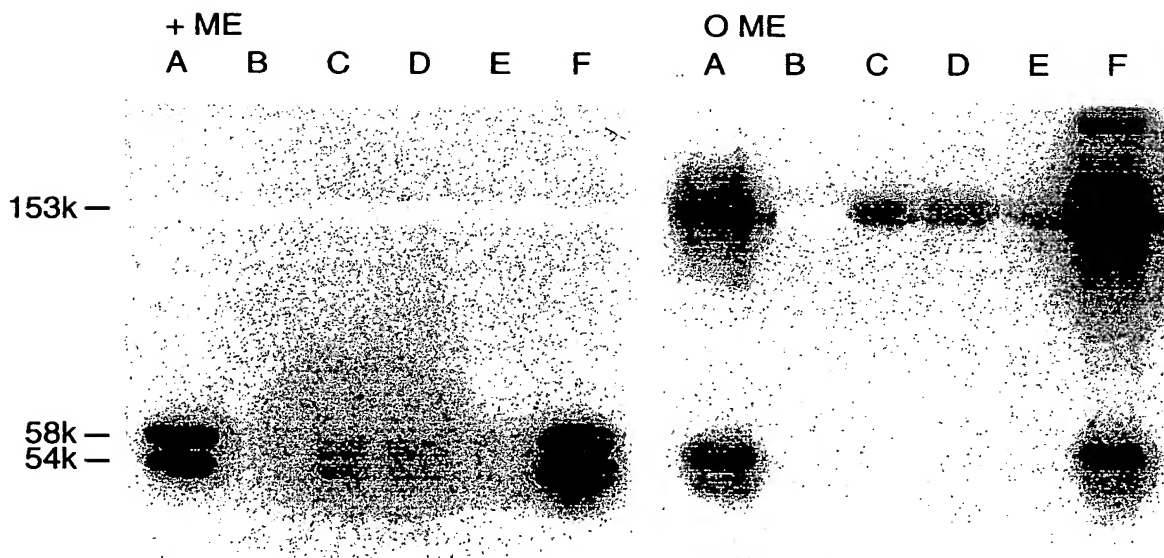


**FIG.\_6B**

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**FIG.\_7**



**FIG.\_8**



FIG.\_9

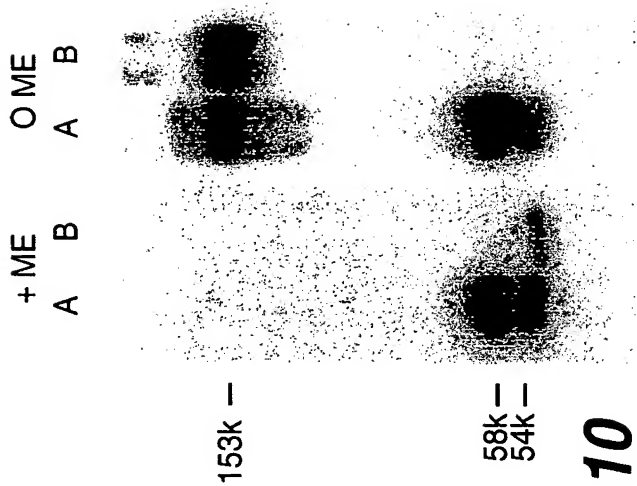
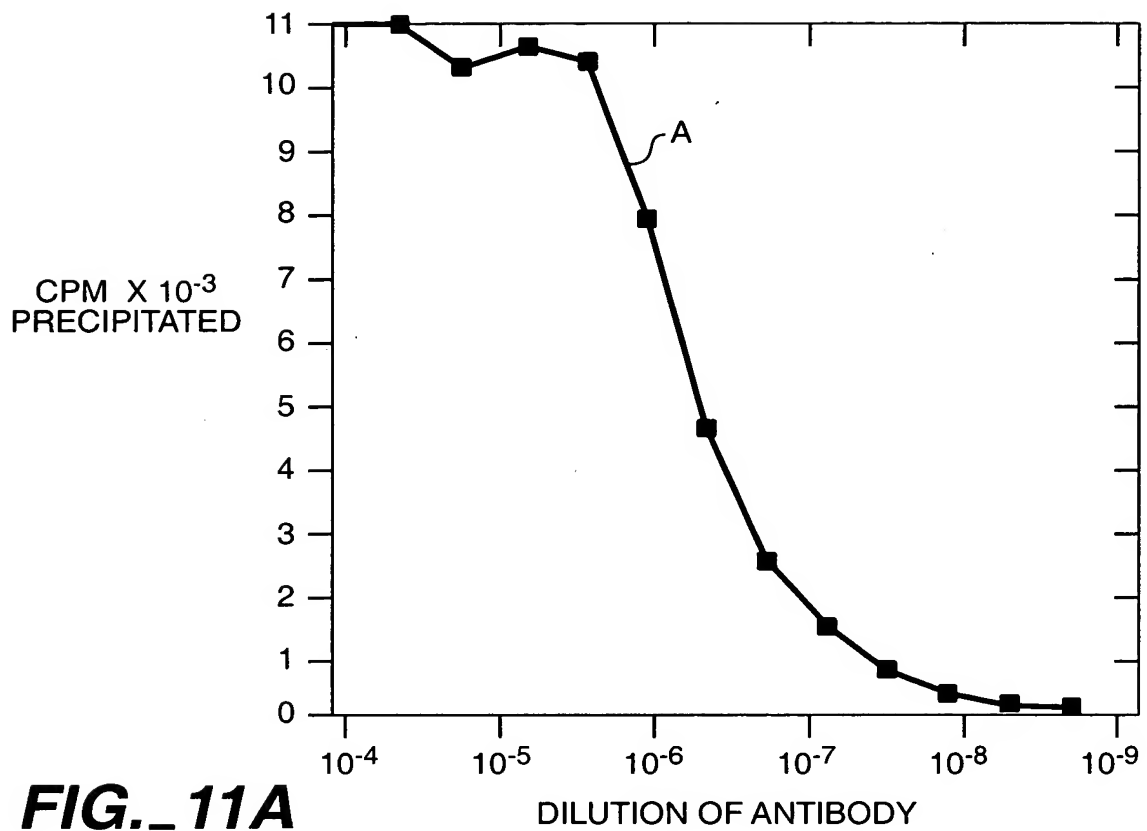


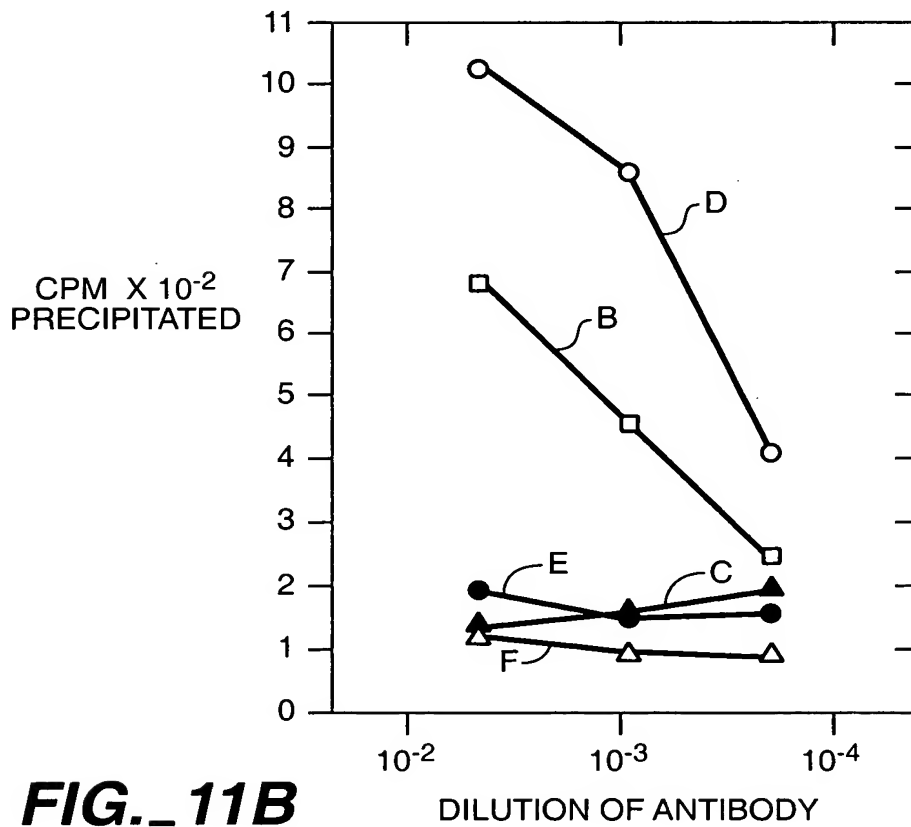
FIG.\_10



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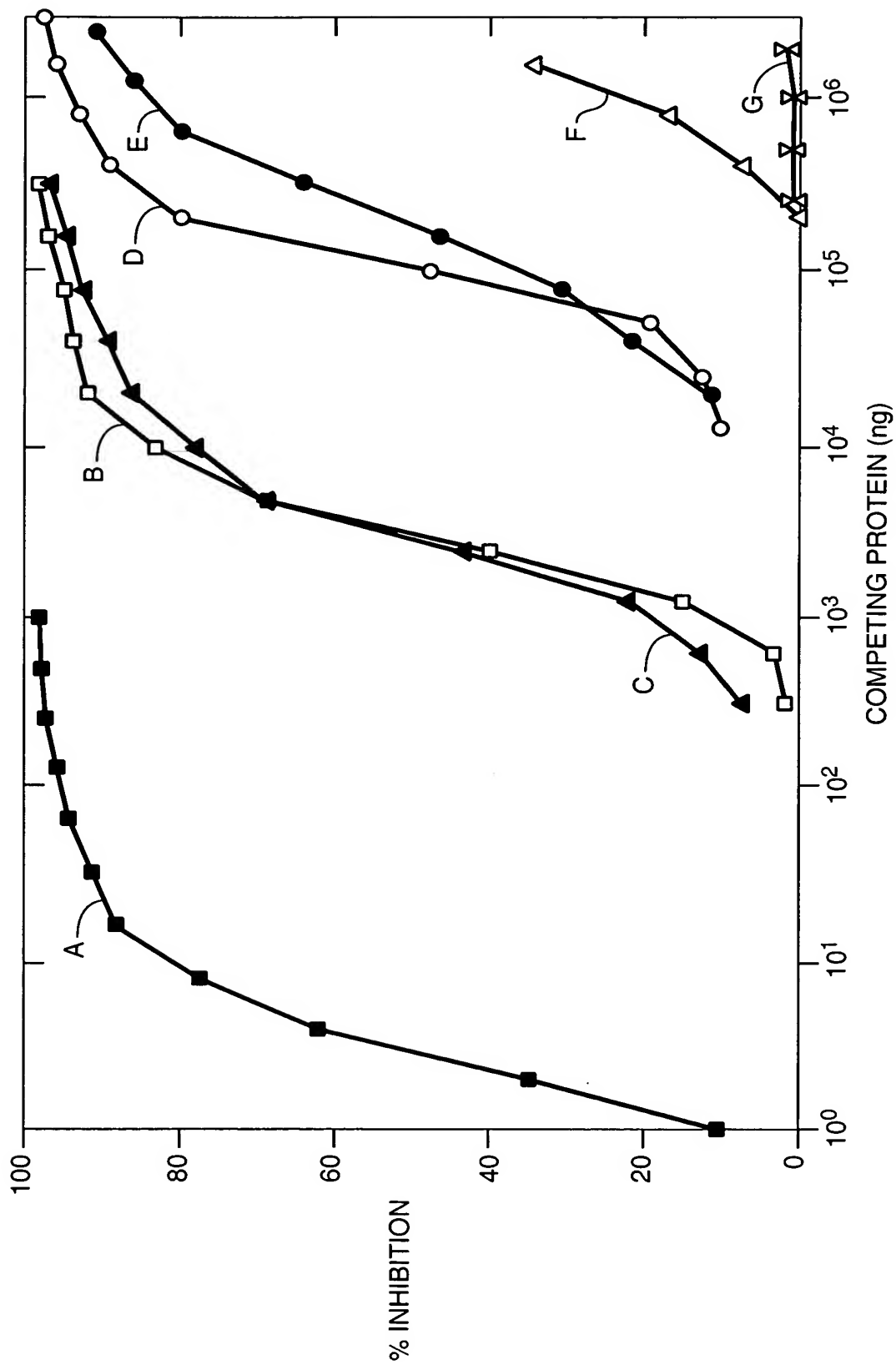


**FIG. 11A**

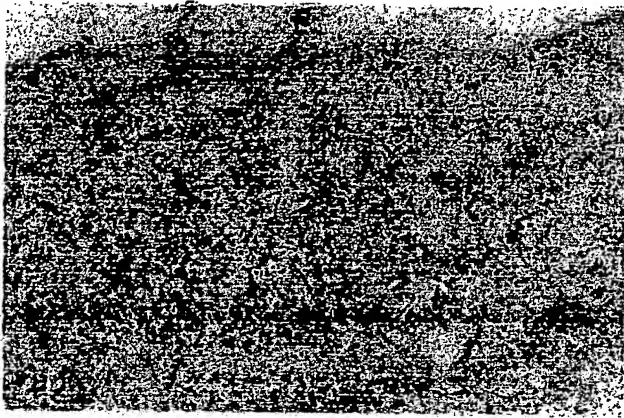


**FIG. 11B**

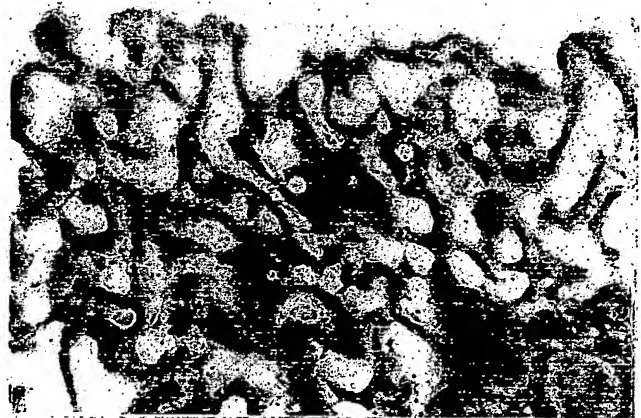
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**FIG. 12**



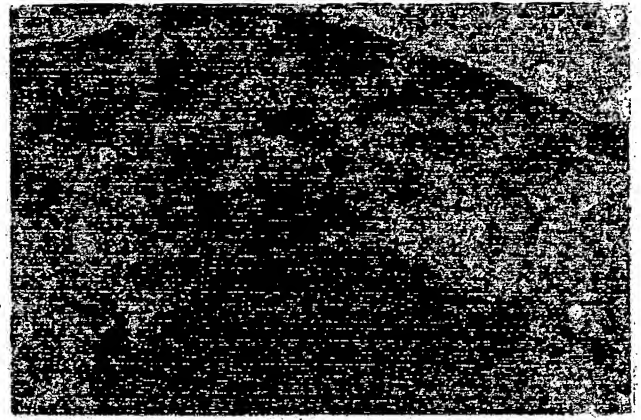
**FIG.\_13A**



**FIG.\_13B**



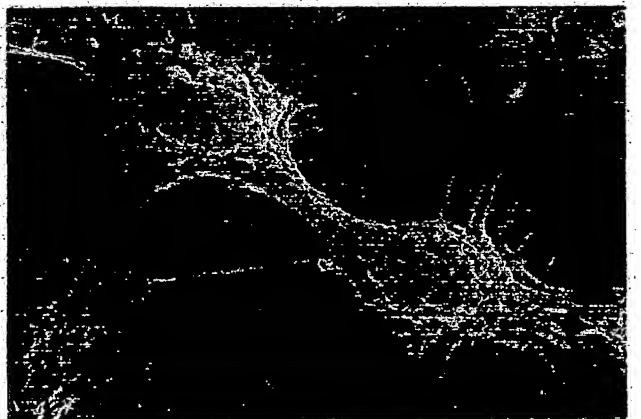
**FIG.\_13C**



**FIG.\_13D**

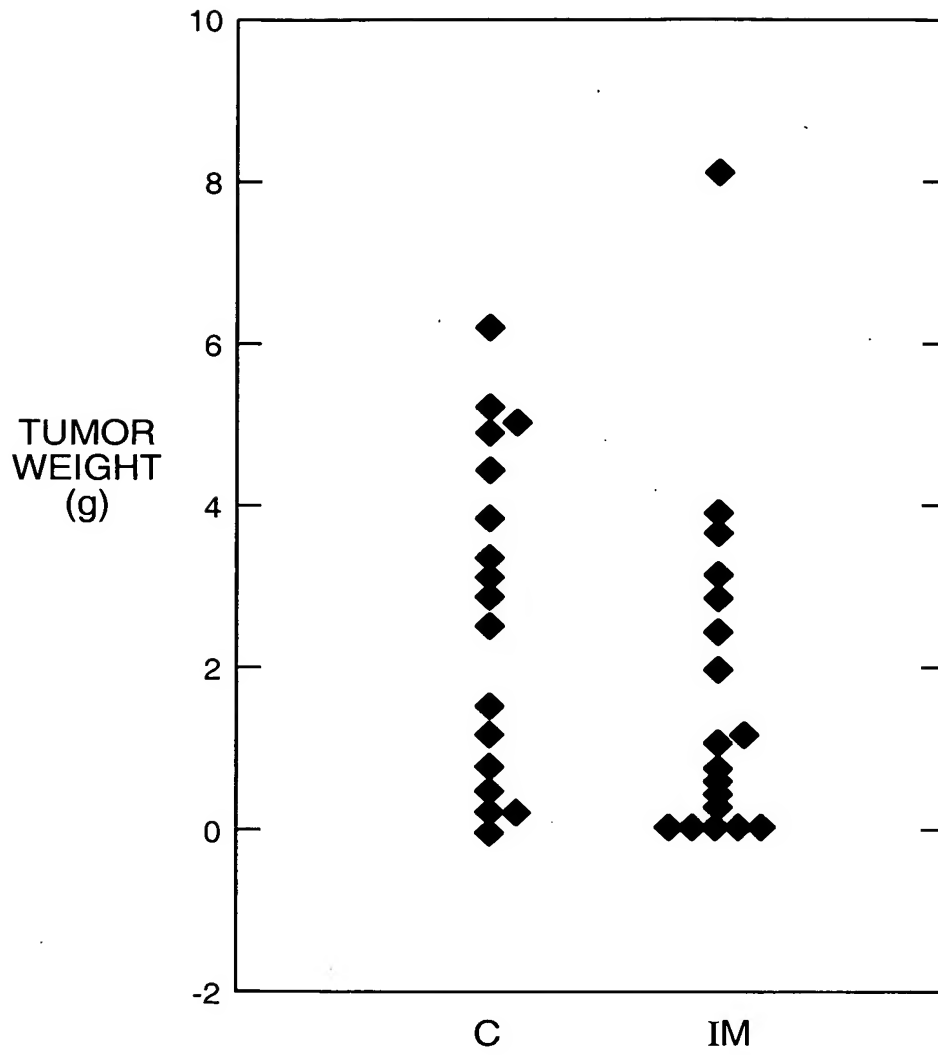


**FIG.\_13E**



**FIG.\_13F**

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**FIG.\_14**

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1	ACA	GTC	AGC	CGC	ATG	GCT	CCC	CTG	TGC	CCC	AGC	CCC	TGG	CTC	CCT	CTG	12
1																	48
13	L	I	P	A	P	A	P	G	L	T	V	Q	L	L	L	S	28
49	TTG	ATC	CCG	GCC	CCT	GCT	CCA	GGC	CTC	ACT	GTG	CAA	CTG	CTG	CTG	TCA	96
29	L	L	L	L	M	P	V	H	P	Q	R	L	P	R	M	Q	44
97	CTG	CTG	CTT	CTG	ATG	CCT	GTC	CAT	CCC	CAG	AGG	TTG	CCC	CGG	ATG	CAG	144
45	E	D	S	P	L	G	G	G	S	S	G	E	D	D	P	L	60
145	GAG	GAT	TCC	CCC	TTG	GGA	GGA	GGC	TCT	TCT	GGG	GAA	GAT	GAC	CCA	CTG	192
61	G	E	E	D	L	P	S	E	E	D	S	P	R	E	E	D	76
193	GGC	GAG	GAG	GAT	CTG	CCC	AGT	GAA	GAG	GAT	TCA	CCC	AGA	GAG	GAG	GAT	240
77	P	P	G	E	E	D	L	P	G	E	E	D	L	P	G	E	92
241	CCA	CCC	GGA	GAG	GAG	GAT	CTA	CCT	GGA	GAG	GAG	GAT	CTA	CCT	GGA	GAG	288
93	E	D	L	P	E	V	K	P	K	S	E	E	E	G	S	L	108
289	GAG	GAT	CTA	CCT	GAA	GTT	AAG	CCT	AAA	TCA	GAA	GAA	GAG	GGC	TCC	CTG	336
109	K	L	E	D	L	P	T	V	E	A	P	G	D	P	Q	E	124
337	AAG	TTA	GAG	GAT	CTA	CCT	ACT	GTT	GAG	GCT	CCT	GGA	GAT	CCT	CAA	GAA	384
125	P	Q	N	N	A	H	R	D	K	E	G	D	D	Q	S	H	140
385	CCC	CAG	AAT	AAT	GCC	CAC	AGG	GAC	AAA	GAA	GGG	GAT	GAC	CAG	AGT	CAT	432
141	W	R	Y	G	G	D	P	P	W	P	R	V	S	P	A	C	156
433	TGG	CGC	TAT	GGA	GGC	GAC	CCG	CCC	TGG	CCC	CGG	GTG	TCC	CCA	GCC	TGC	480
157	A	G	R	F	Q	S	P	V	D	I	R	P	Q	L	A	A	172
481	GCG	GCG	CGC	TTC	CAG	TCC	CCG	GTG	GAT	ATC	CGC	CCC	CAG	CTC	GCC	GCC	528

FIG.\_15A

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173 F C P A L R P L E L L L G F Q L P 188
529 TTC TGC CCG GCC CTG CTG CGC CCC CTG GAA CTC CTG GGC TTC CAG CTC CCG 576

189 P L P E L L R L R N N G H S V Q L 204
577 CCG CTC CCA GAA CTG CGC CTG CGC AAC AAT GGC CAC AGT GTG CAA CTG 624

205 T L P P G L E M A L G P G R E Y 220
625 ACC CTG CCT CCT GGG CTA GAG ATG GCT CTG GGT CCC GGG CGG GAG TAC 672

221 R A L Q L L H L H W G A A G R P G 236
673 CGG GCT CTG CAG CTG CAT CTG CAC TGG GGG GCT GCA GGT CGT CCG GGC 720

237 S E H T V E G H R F P A E I H V 252
721 TCG GAG CAC ACT GTG GAA GGC CAC CGT TTC CTG GGC GAG ATC CAC GTG 768

253 V H L S T A F A A R V D E A L G R 268
769 GTT CAC CTC AGC ACC GCC TTT GCC AGA GTT GAC GAG GCC TTG GGG CGC 816

269 P G G L A V L A A A F L E E G P E 284
817 CCG GGA GGC CTG GCC GTG TTT GGC GCC TTT CTG GAG GAG GGC CCG GAA 864

285 E N S A Y E Q L L S R L E E I A 300
865 GAA AAC AGT GCC TAT GAG CAG CTG TTG CTG TCT CGC TTG GAA GAA ATC GCT 912

301 E E G S E T Q V P G L D I S A L 316
913 GAG GAA GGC TCA GAG ACT CAG GTC CCA GGA CTG GAC ATA TCT GCA CTC 960

317 L P S D F S R Y F Q Q Y E G S L T 332
961 CTG CCC TCT GAC TTC AGC CGC TAC TTC CAA TAT GAG GGG TCT CTG ACT 1008

333 T P P C A Q G V I W T V F N Q T 348
1009 ACA CCG CCC TGT GCC CAG GGT GTC ATC TGG ACT GTG TTT AAC CAG ACA 1056

```

**FIG.\_15B**

349 V M L S A K Q L H T L S D T L W 364  
1057 GTG ATG CTG AGT AGT AAG CAG CTC CAC ACC CTC TCT GAC ACC CTG TGG 1104

365 G P G D S R L Q L N F R A T Q P 380  
1105 GGA CCT GGT GAC TCT CGG CTA CAG CTG AAC TTC CGA GCG ACG CAG CCT 1152

381 L N G R V I E A S F P A G V D S 396  
1153 TTG AAT GGG CGA GTG ATT GAG GCC TCC TTC CCT GCT GGA GTG GAC AGC 1200

397 S P R A A E P V Q L N S C L A A 412  
1201 AGT CCT CGG GCT GCT GAG CCA GTC CAG CTG AAT TCC TGC CTG GCT GCT 1248

413 G D I L A L V F G L L F A V T S 428  
1249 GGT GAC ATC CTA GCC CTG GTC GTT TTT GGC CTC CTT TTT GCT GTC ACC AGC 1296

429 V A F L L V Q M R R Q H R R G T K 444  
1297 GTC GCG TTC CTT GTG CAG ATG AGA AGG CAG CAC AGA AGG GGA ACC AAA 1344

445 G G V S Y R P A E V A E T G A \* 460  
1345 GGG GGT GTG AGC TAC CGC CCA GCA GAG GTA GCC GAG ACT GGA GCC TAG 1392

1393 AGG CTG GAT CTT GGA GAA TGT GAG AAG CCA GCC AGA GGC ATC TGA GGG 1440

1441 GGA GCC GGT AAC TGT CCT GTC CTC ATT ATG CCA CTT CCT TTT AAC 1488

1489 TGC CAA GAA ATT TTT TAA AAT TAT TTA TAA T 1522

FIG.\_15C

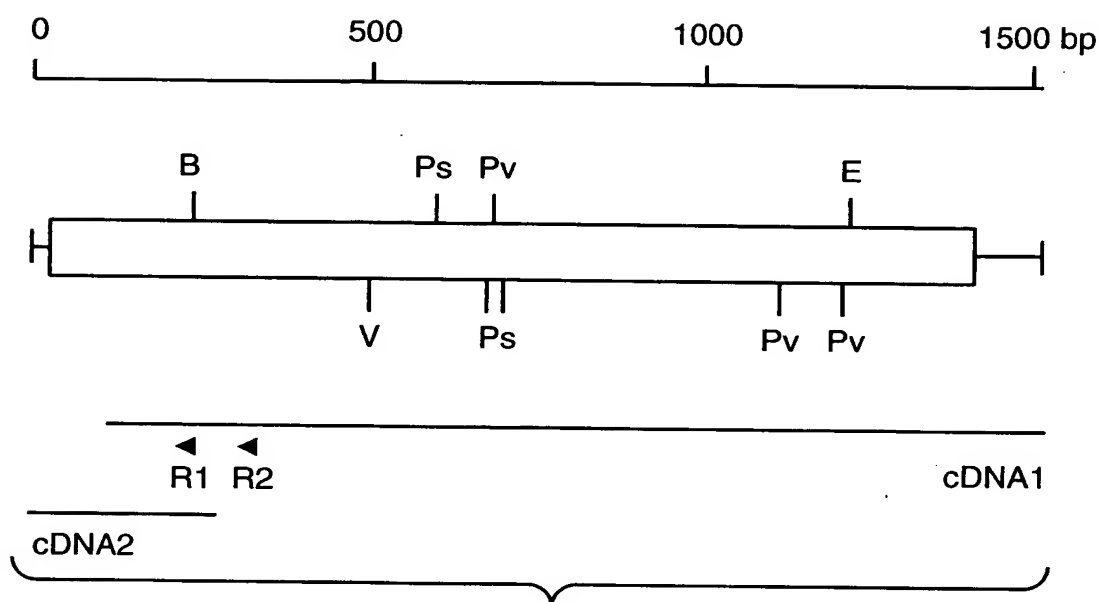
FIG.\_15

FIG.\_15A

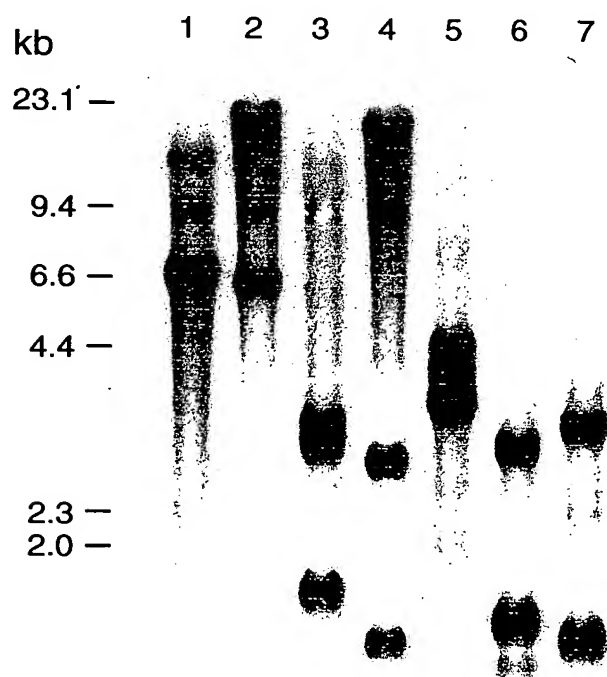
FIG.\_15B

FIG.\_15C

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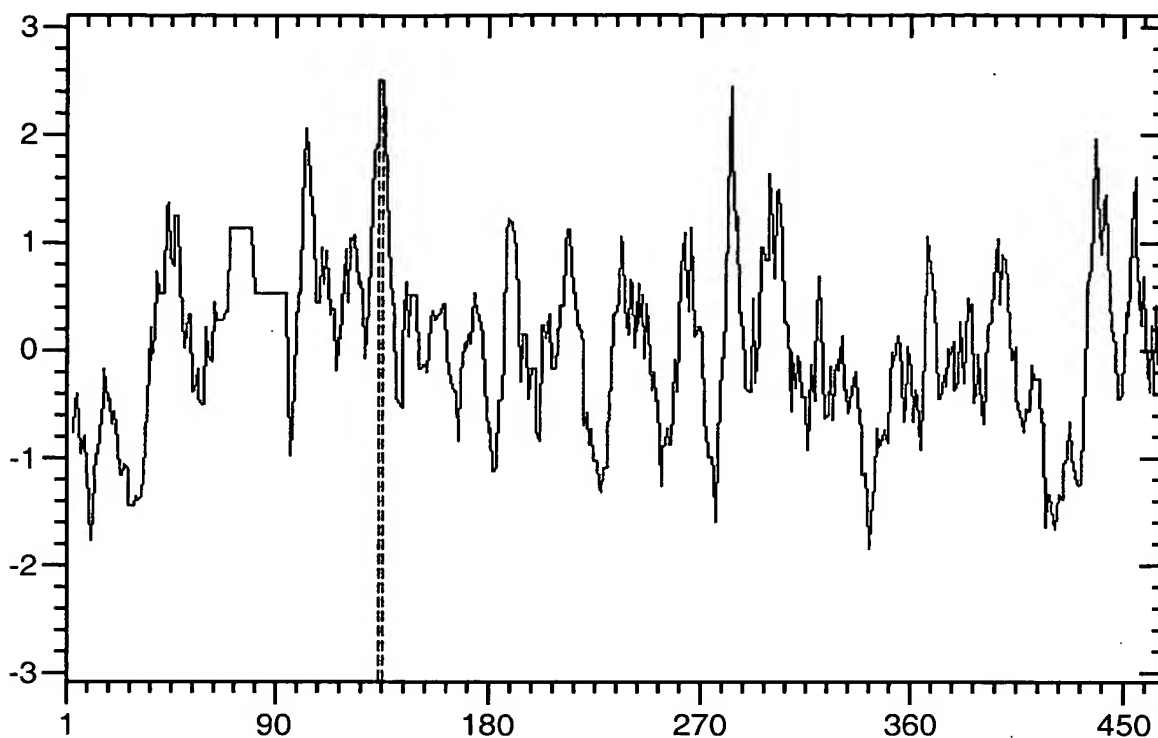
**FIG.\_16**



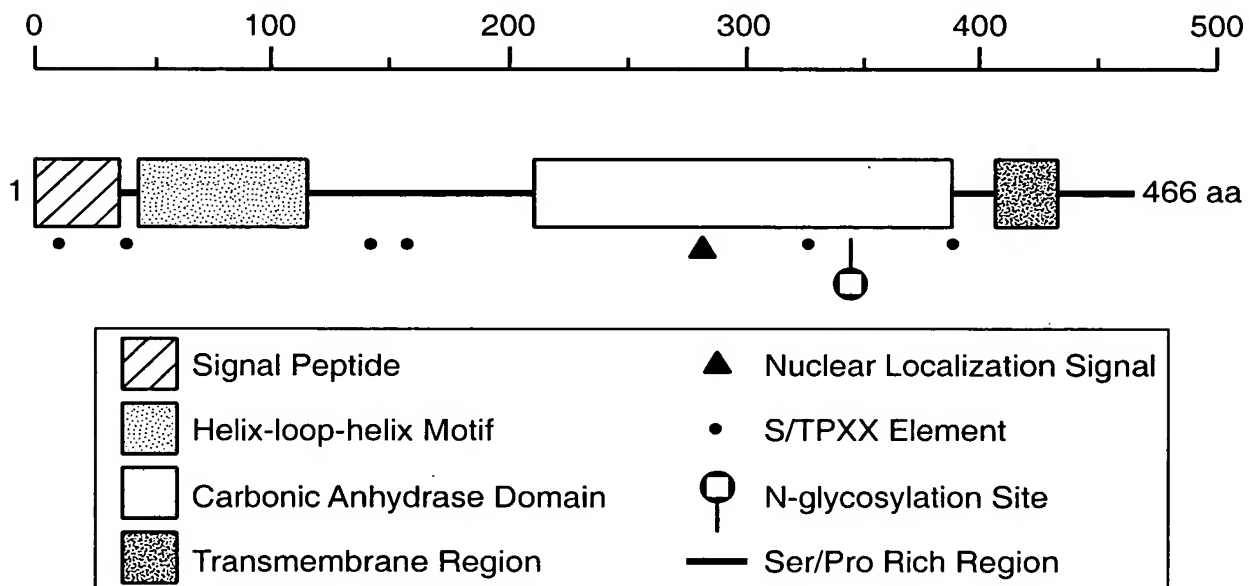
**FIG.\_17**



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**FIG.\_18**



**FIG.\_19D**

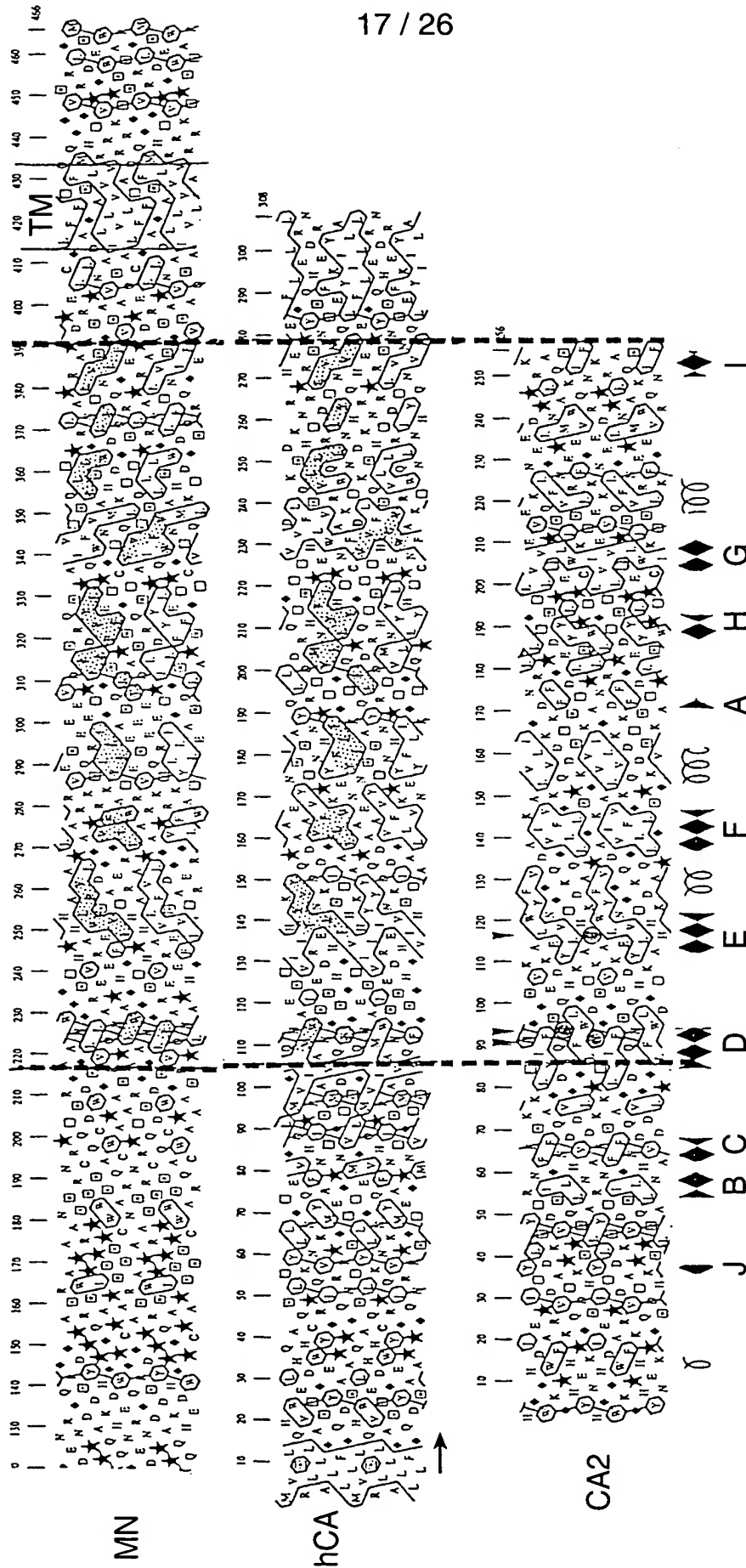


FIG.-19A

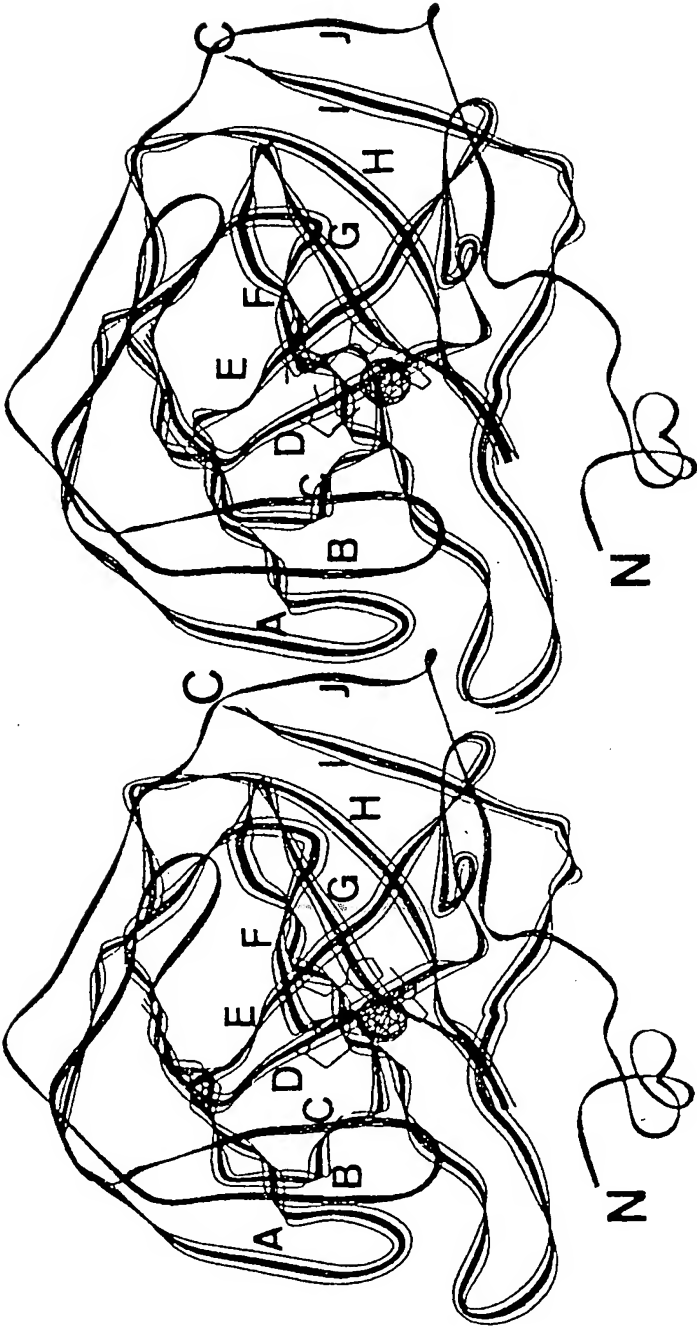


FIG.-19B



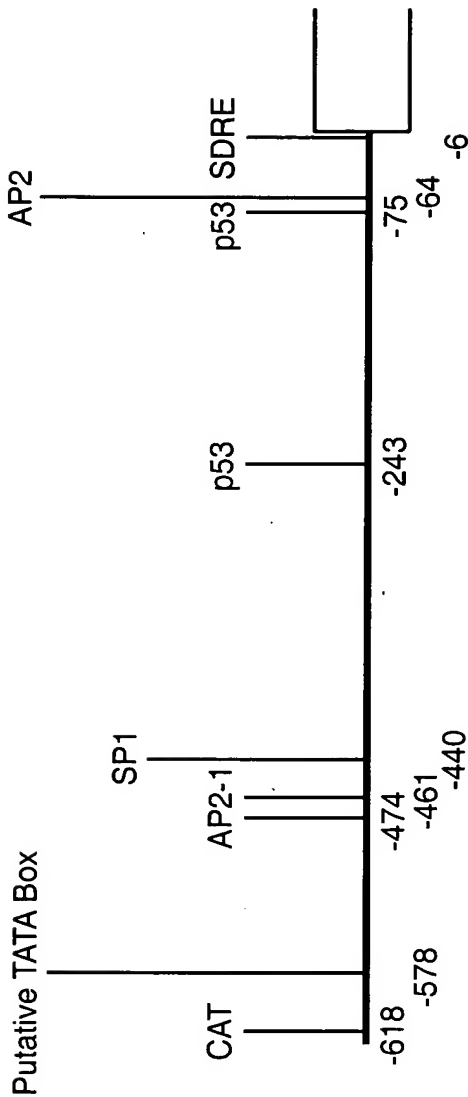


FIG.\_20

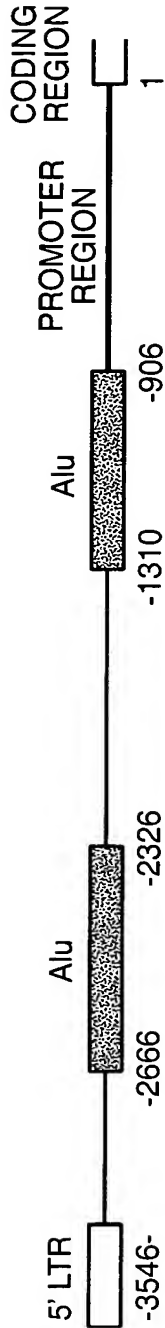
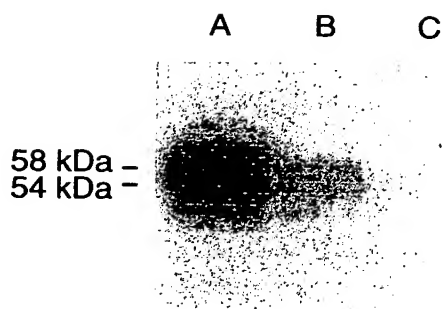
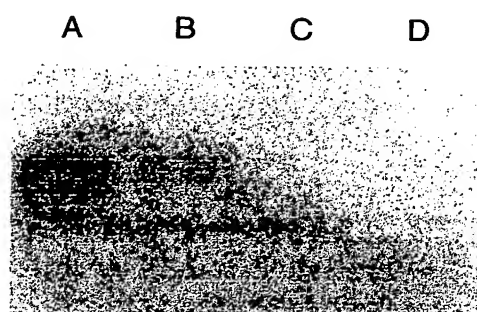


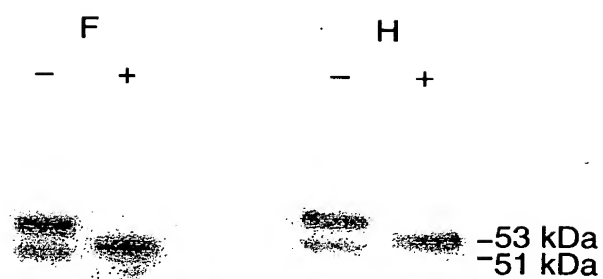
FIG.\_21



**FIG.\_22A**

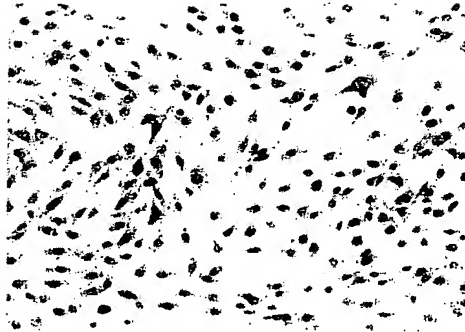


**FIG.\_22B**

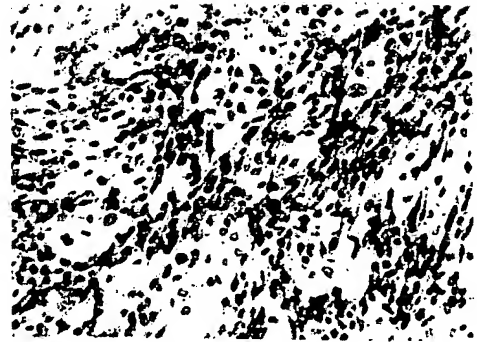


**FIG.\_22C**

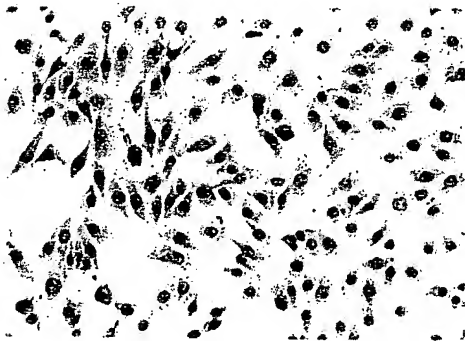
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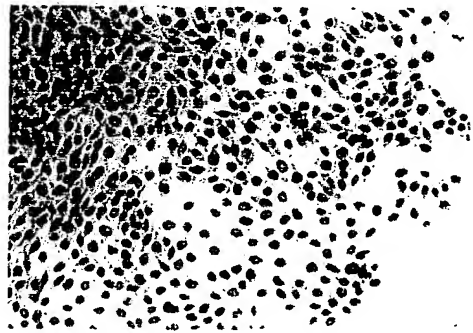
**FIG.\_23A**



**FIG.\_23B**



**FIG.\_23C**



**FIG.\_23D**



**FIG.\_23E**

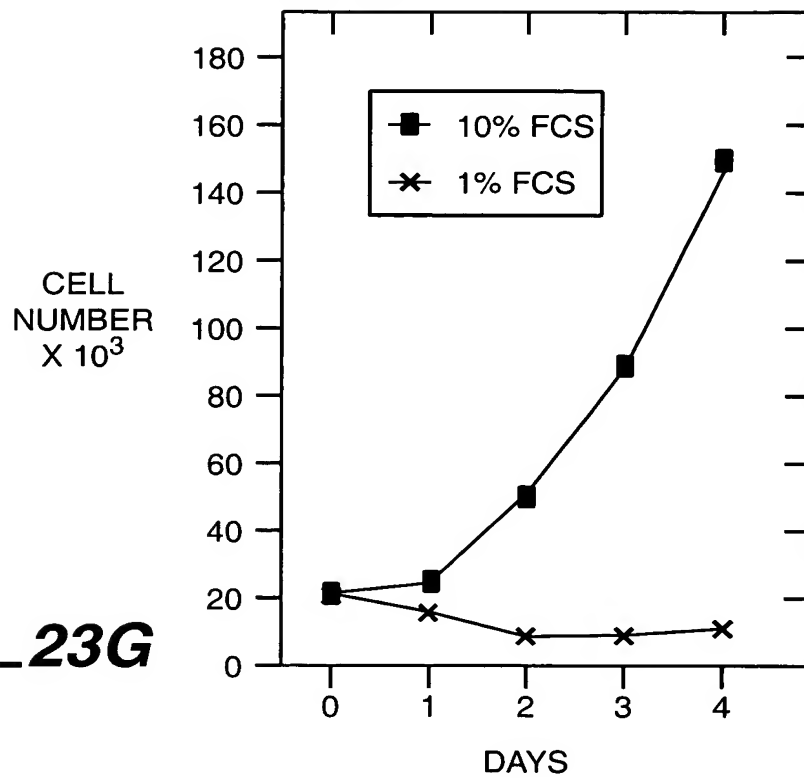


**FIG.\_23F**

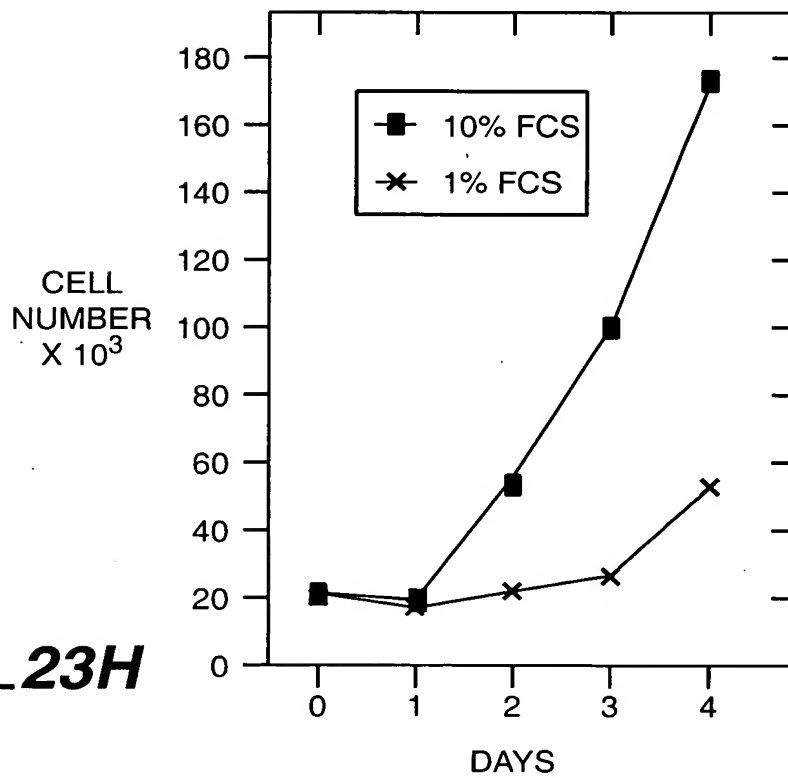


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**FIG.\_23G**

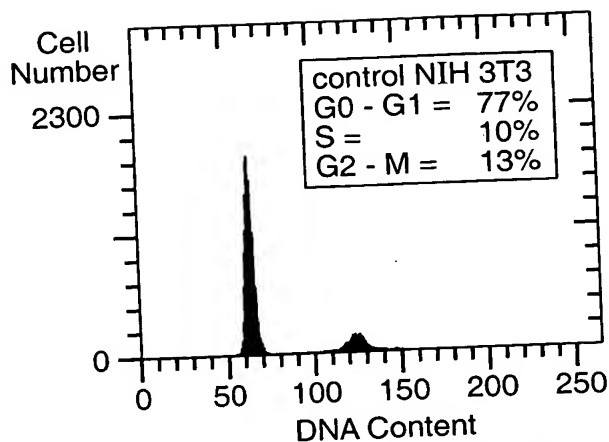


**FIG.\_23H**

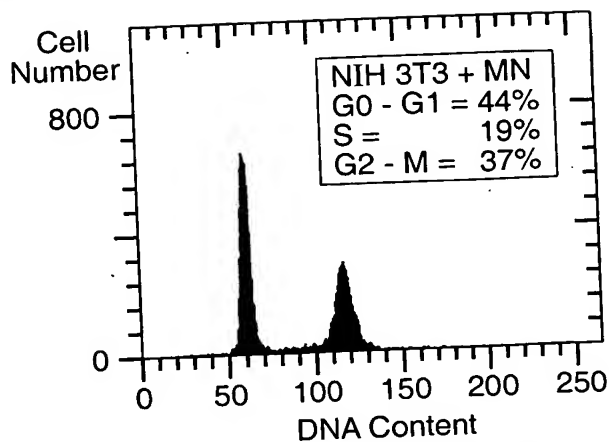




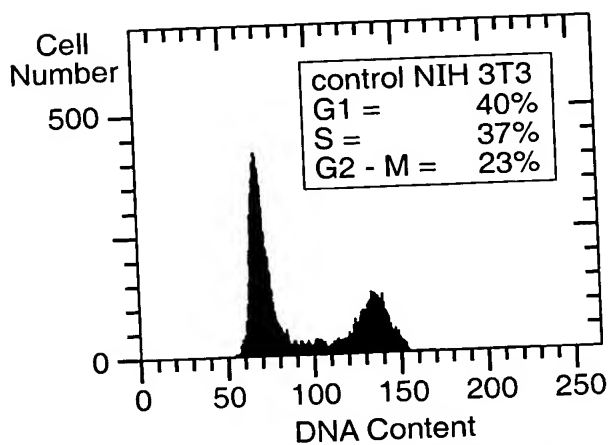
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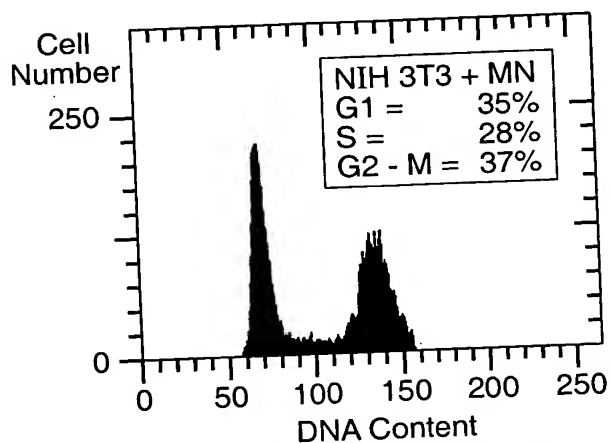
**FIG.\_24A-1**



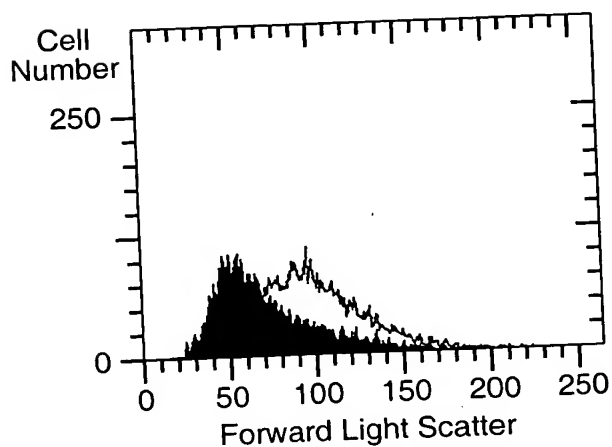
**FIG.\_24A-2**



**FIG.\_24B-1**



**FIG.\_24B-2**



■ NIH 3T3 + MN  
□ CONTROL NIH 3T3

— Kolmogorov-Smirnov Statistics —  
D/s(n) = 19.03  
D = 0.36  
Channel = 70  
Channels 0 - 255  
99% probability of difference

**FIG.\_24C**

SQ Sequence 5052 BP: 1201 A; 1249 C; 1201 G; 1399 T.

```

GGATCCTGTT GACTCGTGAC CTTACCCCCA ACCCTGTGCT CTCTGAAACA TGAGCTGTGT
CCACTCAGGG TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGT TAAA CAGATGCTTG
AAGGCAGCAT GCTCGTTAAG AGTCATCACC AATCCCTAAT CTCAAGTAAT CAGGGACACA
AACACTGCGG AAGGCCGCAG GGTCTCTGCT CTAGGAAAAC CAGAGACCTT TGTTCACTTG
TTTATCTGAC CTTCCCTCCA CTATTGTCCA TGACCCTGCC AAATCCCCCT CTGTGAGAAA
CACCCAAGAA TTATCAATAA AAAAATAAAT TTAATAAAAA AATACAAAAA AAAAAAAAAA
AAAAAAAAAA GACTTACGAA TAGTTATTGA TAAATGAATA GCTATTGGTA AAGCCAAGTA
AATGATCATA TTCAAACCA GACGGCCATC ATCACAGCTC AAGTCTACCT GATTTGATCT
CTTTATCATT GTCATTCTTT GGATTCACTA GATTAGTCAT CATCCTCAA ATTCTCCCCC
AAGTTCTAAT TACGTTCCAA ACATTTAGGG GTTACATGAA GCTTGAACCT ACTACCTTCT
TTGCTTTTGA GCCATGAGTT GTAGGAATGA TGAGTTTACA CCTTACATGC TGGGGATTAA
TTTAACTTT ACCTCTAAGT CAGTTGGGTA GCCTTTGGCT TATTTTTGTA GCTAATTTTG
TAGTTAATGG ATGCACTGTG AATCTTGCTA TGATAGTTTT CCTCCACACT TTGCCACTAG
GGGTAGGTAG GTACTCAGTT TTCAGTAATT GCTTACCTAA GACCCTAAGC CCTATTTCTC
TTGTACTGGC CTTTATCTGT AATATGGGCA TATTTAATAC AATATAATTT TTGGAGTTTT
TTTGTGTTGTT TGTTTGTGTTG TTTTTTTGAG ACGGAGTCTT GCATCTGTCA TGCCCAGGCT
GGAGTAGCAG TGGTGCCATC TCGGCTCACT GCAAGCTCCA CCTCCCGAGT TCACGCCATT
TTCTTGCCCTC AGCCTCCCGA GTAGCTGGGA CTACAGGCGC CCGCCACCAT GCCCGGCTAA
TTTTTTGTAT TTTTGGTAGA GACGGGGTTT CACCGTGTTA GCCAGAATGG TCTCGATCTC
CTGACTTCGT GATCCACCCG CCTCGGCCTC CCAAAGTTCT GGGATTACAG GTGTGAGCCA
CCGCACCTGG CCAATTTTTT GAGTCTTTTA AAGTAAAAAT ATGTCTTGTA AGCTGGTAAC
TATGGTACAT TTCCTTTTAT TAATGTGGTG CTGACGGTCA TATAGGTTCT TTTGAGTTTG
GCATGCATAT GCTACTTTTT GCAGTCCTTT CATTACATTT TTCTCTCTTC ATTTGAAGAG
CATGTTATAT CTTT TAGCTT CACTTGGCTT AAAAGGTTCT CTCATTAGCC TAACACAGTG
TCATTGTTGG TACCACTTGG ATCATAAGTG GAAAAACAGT CAAGAAATTG CACAGTAATA
CTTGTTTGTA AGAGGGATGA TTCAGGTGAA TCTGACACTA AGAACTCCC CTACCTGAGG
TCTGAGATTC CTCTGACATT GCTGTATATA GGCTTTTCCT TTGACAGCCT GTGACTGCGG
ACTATTTTTC TTAAGCAAGA TATGCTAAAG TTTTGTGAGC CTTTTTCCAG AGAGAGGTCT
CATATCTGCA TCAAGTGAGA ACATATAATG TCTGCATGTT TCCATATTT AGGAATGTTT
GCTTGTTGTTT TATGCTTTTA TATAGACAGG GAAACTTGTT CCTCAGTGAC CCAAAGAGG
TGGGAATTGT TATTGGATAT CATCATTGGC CCACGCTTTC TGACCTTGGA AACAATTAAG
GGTTCATAAT CTCAATTCTG TCAGAATTGG TACAAGAAAT AGCTGCTATG TTTCTTGACA
TTCCACTTGG TAGGAAATAA GAATGTGAAA CTCTTCAGTT GGTGTGTGTC CCTNGTTTTT
TTGCAATTTT CTTCTTACTG TGTTAAAAAA AAGTATGATC TTGCTCTGAG AGGTGAGGCA
TTCTTAATCA TGATCTTTAA AGATCAATAA TATAATCCTT TCAAGGATTA TGTCTTTATT
ATAATAAAGA TAATTTGTCT TTAACAGAAT CAATAATATA ATCCCTTAAA GGATTATATC
TTTGCTGGGC GCAGTGGCTC ACACCTGTAA TCCCAGCACT TTGGGTGGCC AAGGTGGAAG
GATCAAATTT GCCTACTTCT ATATTATCTT CTAAAGCAGA ATTCATCTCT CTTCCCTCAA
TATGATGATA TTGACAGGGT TTGCCCTCAC TCACTAGATT GTGAGCTCCT GCTCAGGGCA
GGTAGNGTTT TTTGTTTTTG TTTTGTGTTT TCTTTTTTGA GACAGGGTCT TGCTCTGTCA
CCCAGGCCAG AGTGCAATGG TACAGTCTCA GCTCACTGCA GCCTCAACGC CTCGGCTCAA
ACCATCATCC CATTTAGCC TCCTGAGTAG CTGGGACTAC AGGCACATGC CATTACACCT

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**FIG. 25A**

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GGCTAATTTT TTTGTATTTT TAGTAGAGAC AGGGTTTGGC CATGTTGCCC GGGCTGGTCT
CGAACTCCTG GACTCAAGCA ATCCACCCAC CTCAGCCTCC CAAAATGAGG GACCGTGTCT
TATTCATTTT CATGTCCCTA GTCCATAGCC CAGTGCTGGA CCTATGGTAG TACTAAATAA
ATATTTGTTG AATGCAATAG TAAATAGCAT TTCAGGGAGC AAGAACTAGA TTAACAAAGG
TGGTAAAAGG TTTGGAGAAA AAAATAATAG TTTAATTTGG CTAGAGTATG AGGGAGAGTA
GTAGGAGACA AGATGGAAAG GTCTCTTGGG CAAGGTTTTG AAGGAAGTTG GAAGTCAGAA
GTACACAATG TGATATCGTG GCAGGCAGTG GGGAGCCAAT GAAGGCTTTT GAGCAGGAGA
GTAATGTGTT GAAAAATAAA TATAGGTTAA ACCTATCAGA GCCCCTCTGA CACATACACT
TGCTTTTCAT TCAAGCTCAA GTTTGTCTCC CACATACCCA TTACTTAACT CACCCTCGGG
CTCCCCTAGC AGCCTGCCCT ACCTCTTTAC CTGCTTCCTG GTGGAGTCAG GGATGTATAC
ATGAGCTGCT TTCCCTCTCA GCCAGAGACA TGGGGGGCCC CAGCTCCCCT GCCTTTCCCC
TTCTGTGCCCT GGAGCTGGGA AGCAGGCCAG GGTAGCTGA GGCTGGCTGG CAAGCAGCTG
GGTGGTGCCA GGGAGAGCCT GCATAGTGCC AGGTGGTGCC TTGGGTTCCA AGCTAGTCCA
TGGCCCCGAT AACCTTCTGC CTGTGCACAC ACCTGCCCTT CACTCCACCC CCATCCTAGC
TTTGGTATGG GGGAGAGGGC ACAGGGCCAG ACAAACCTGT GAGACTTTGG CTCCATCTCT
GCAAAAGGGC GCTCTGTGAG TCAGCTGTCT CCCCTCCAGG CTTGCTCCTC CCCACCCAG
CTCTCGTTTC CAATGCACGT ACAGCCCGTA CACACCGTGT GCTGGGACAC CCCACAGTCA
GCGCATGGCT CCCCTGTGCC CCAGCCCCTG GCTCCCTCTG TTGATCCCGG CCCCTGCTCC
AGGCCTCACT GTGCAACTGC TGCTGTCACT GCTGCTTCTG ATGCCTGTCC ATCCCAGAG
GTTGCCCCGG ATGCAGGAGG ATTCCCCCTT GGAGGAGGCT CTTCTGGGGA AGATGACCCA
CTGGGCGAGG AGGATCTGCC CAGTGAAGAG GATTCACCCA GAGAGGAGGA TCCACCCGGA
GAGGAGGATC TACCTGGAGA GGAGGATCTA CCTGGAGAGG AGGATCTACC TGAAGTTAAT
GCCTAAATCA GAAGAAGAGG GCTCCCTGAA GTTAGAGGAT CTACCTACTG TTGAGGCTCC
TGGAGATCCT CAAGAACCCC AGAATAATGC CCACAGGGAC AAAGAAGGGG ATGACCAGAG
TCATTGGCGC TATGGAGGCG ACCCGCCTGG CCCCGGGTGT CCCCAGCCTG CGCGGGCCGC
TTCCAGTCCC CGGTGGATAT CCGCCCCCAG CTCGCCGCCT TCTGCCCGGC CCTGCGCCCC
CTGGAACTCC TGGGCTTCCA GCTCCCGCCG CTCCCAGAAC TCGCCTGCA GACAATGGCC
ACAGTGTGCA ACTGACCCTG CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT
ACCGGCTCTG CAGCTGCATC TGCCTGGGG GGCTGCAGGT CGTCCGGGCT CGGAGCACAC
TGTGGAAGGC CACCGTTTCC CTGCGGAGAT CCACGTGGTT CACCTCAGCA CCGCCTTTGC
CAGAGTTGAC GAGGCCTTGG GGCGCCCGGG AGGCCTGGCC GTGTTGGCGC CTTTCTGGAG
GAGGGCCCCG AAGAAAACAG TGTCTATGA GCAGTTGCTG TCTCGCTTGG AAGAAATCGC
TGAGGAAGGC TCAGAGACTC AGGTCCCAGG ACTGGACATA TCTGCACTCC TGCCCTCTGA
CTTCAGCCGC TACTTCCAAT ATGAGGGGTC TCTGACTACA CCGCCCTGTG CCCAGGGTGT
CATCTGGACT GTGTTTAACC AGACAGTGAT GCTGAGTGCT AAGCAGCTCC ACACCCTCTC
TGACACCCTG TGGGGACCTG GTGACTCTCG GCTACAGCTG AACTTCCGAG CGACGCAGCC
TTTGAATGGG CGAGTGATTG AGGCCTCCTT CCCTGCTGGA GTGGACAGCA GTCCTCGGGC
TGCTGAGCCA GTCCAGCTGA ATTCTGCCT GGCTGCTGGT GACATCCTAG CCTGGGTTTT
TGGCCTCCTT TTTGCTGTCA CCAGCGTCGC GTTCCTTGTG CAGATGAGAA GGCAGCACAG
AAGGGGAACC AAAGGGGGTG TGAGCGTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT
AGAGGCTGGA TCTTGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA
ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA
AATATTTATA AT

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**FIG. 25B**